

## SEQUENCE LISTING

&lt;110&gt; Cargill Incorporated

&lt;120&gt; ALANINE 2, 3-AMINOMUTASE

&lt;130&gt; 63358

&lt;150&gt; US 60/350,727

&lt;151&gt; 2002-01-18

&lt;150&gt; US 60/375,785

&lt;151&gt; 2002-04-25

&lt;160&gt; 66

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 40

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; PCR primer

&lt;400&gt; 1

gcgcgaggag gagttcatat gaaaaacaaa tggataaac

40

&lt;210&gt; 2

&lt;211&gt; 36

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; PCR primer

&lt;400&gt; 2

cgggcaccgc ttcgaggcgg ccgcaccatt cgcgatg

36

&lt;210&gt; 3

&lt;211&gt; 1416

&lt;212&gt; DNA

&lt;213&gt; Bacillus subtilis

&lt;400&gt; 3

ttgaaaaaca aatggtataa accgaaacgg cattggaagg agatcgagtt atggaaggac 60

gttcggaag agaaatggaa cgattggctt tggcagctga cacacactgt aagaacgtta 120

gatgatttaa agaaagtcac taatctgacc gaggatgaag aggaaggcgt cagaatttct 180

acaaaaacga tccccttaaa tattacacct tactatgctt ctttaatgga ccccgacaat 240

ccgagatgcc cggtagcat gcagtctgtg ccgctttctg aagaaatgca caaaacaaaa 300

tacgatctgg aagacccgct tcatgaggat gaagattcac cggtagccgg tctgacacac 360

cgctatcccg accgtgtgct gtttcttctg acgaatcaat gttccatgta ctgccgctac 420

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tgcacaagaa ggcgcttttc cggacaaatc ggaatgggcg tccccaaaaa acagcttgat      480
gctgcaattg cttatatccg ggaaacaccc gaaatccgcg attgtttaat ttcaggcggt      540
gatgggctgc tcatcaacga ccaaatttta gaatatattt taaaagagct gcgcagcatt      600
ccgcatctgg aagtcacag aatcggaaca agagctcccg tcgtctttcc gcagcgcat      660
accgatcatc tgtgcgagat attgaaaaaa tatcatccgg tctggctgaa caccatttt      720
aacacaagca tcgaaatgac agaagaatcc gttgaggcat gtgaaaagct ggtgaacgcg      780
ggagtgccgg tcggaaatca ggctgtcgta ttagcaggta ttaatgattc ggttccaatt      840
atgaaaaagc tcatgcatga cttggtaaaa atcagagtcc gtccttatta tatttaccaa      900
tgtgatctgt cagaaggaat agggcatttc agagctcctg tttccaaagg tttggagatc      960
attgaagggc tgagaggcca tacctcaggc tatgcggttc ctacctttgt cgttgacgca     1020
ccaggcggag gaggtaaaat cgccctgcag ccaaactatg tcctgtcaca aagtcctgac     1080
aaagtgatct taagaaattt tgaagggtgtg attacgtcat atccggaacc agagaattat     1140
atccccaatc aggcagacgc ctattttgag tccgttttcc ctgaaaccgc tgacaaaaag     1200
gagccgatcg ggctgagtgc catttttgct gacaaagaag tttcgtttac acctgaaaat     1260
gtagacagaa tcaaaaggag agaggcatac atcgcaaatc cggagcatga aacattaaaa     1320
gatcggcggtg agaaaagaga tcagctcaaa gaaaagaaat ttttggcgca gcagaaaaaa     1380
cagaaagaga ctgaatgcgg aggggattct tcatga                                  1416

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<210> 4  
 <211> 60  
 <212> DNA  
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<220>  
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<210> 5  
 <211> 60  
 <212> DNA  
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<220>  
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<400> 5
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<210> 6

<211> 20  
 <212> DNA  
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<220>  
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<400> 6  
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20

<210> 7  
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 <212> DNA  
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<220>  
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<400> 7  
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20

<210> 8  
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<220>  
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<210> 9  
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<220>  
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51

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<212> DNA  
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<220>  
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<400> 12  
gaatcaatgt tccgtatact gccgctac 28

<210> 13  
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<220>  
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<211> 31  
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<220>  
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<400> 14  
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<220>  
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<213> Artificial Sequence

<220>

<223> PCR primer

<220>

<221> misc\_feature

<222> (1)..(23)

<223> y is t/u or c; s is g or c; b is g, c or t/u.

<400> 16

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23

<210> 17

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<220>

<221> misc\_feature

<222> (1)..(20)

<223> y is t/u or c; s is g or c; b is g, c or t/u; w is a or t/u; n is  
a, c, g or t/u.

<400> 17

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20

<210> 18

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<220>

<221> misc\_feature

<222> (1)..(21)

<223> y is t/u or c; r is g or a; n is a, c, g or t/u.

<400> 18

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21

<210> 19

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 19

ggttttacgag ggcgagaacg gcttgct

27

<210> 20  
 <211> 1416  
 <212> DNA  
 <213> Bacillus subtilis

<220>  
 <221> CDS  
 <222> (1) .. (1416)  
 <223>

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 Met Lys Asn Lys Trp Tyr Lys Pro Lys Arg His Trp Lys Glu Ile Glu  
 1 5 10 15

tta tgg aag gac gtt ccg gaa gag aaa tgg aac gat tgg ctt tgg cag 96  
 Leu Trp Lys Asp Val Pro Glu Glu Lys Trp Asn Asp Trp Leu Trp Gln  
 20 25 30

ctg aca cac act gta aga acg tta gat gat tta aag aaa gtc att aat 144  
 Leu Thr His Thr Val Arg Thr Leu Asp Asp Leu Lys Lys Val Ile Asn  
 35 40 45

ctg acc gag gat gaa gag gaa ggc gtc aga att tct acc aaa acg atc 192  
 Leu Thr Glu Asp Glu Glu Glu Gly Val Arg Ile Ser Thr Lys Thr Ile  
 50 55 60

ccc tta aat att aca cct tac tat gct tct tta atg gac ccc gac aat 240  
 Pro Leu Asn Ile Thr Pro Tyr Tyr Ala Ser Leu Met Asp Pro Asp Asn  
 65 70 75 80

ccg aga tgc ccg gta cgc atg cag tct gtg ccg ctt tct gaa gaa atg 288  
 Pro Arg Cys Pro Val Arg Met Gln Ser Val Pro Leu Ser Glu Glu Met  
 85 90 95

cac aaa aca aaa tac gat atg gaa gac ccg ctt cat gag gat gaa gat 336  
 His Lys Thr Lys Tyr Asp Met Glu Asp Pro Leu His Glu Asp Glu Asp  
 100 105 110

tca ccg gta ccc ggt ctg aca cac cgc tat ccc gac cgt gtg ctg ttt 384  
 Ser Pro Val Pro Gly Leu Thr His Arg Tyr Pro Asp Arg Val Leu Phe  
 115 120 125

ctt gtc acg aat caa tgt tcc gtg tac tgc cgc tac tgc aca aga agg 432  
 Leu Val Thr Asn Gln Cys Ser Val Tyr Cys Arg Tyr Cys Thr Arg Arg  
 130 135 140

cgc ttt tcc gga caa atc gga atg ggc gtc ccc aaa aaa cag ctt gat 480  
 Arg Phe Ser Gly Gln Ile Gly Met Gly Val Pro Lys Lys Gln Leu Asp  
 145 150 155 160

gct gca att gct tat atc cgg gaa aca ccc gaa atc cgc gat tgt tta 528  
 Ala Ala Ile Ala Tyr Ile Arg Glu Thr Pro Glu Ile Arg Asp Cys Leu  
 165 170 175

att tca ggc ggt gat ggg ctg ctc atc aac gac caa att tta gaa tat 576  
 Ile Ser Gly Gly Asp Gly Leu Leu Ile Asn Asp Gln Ile Leu Glu Tyr

180										185										190									
att	tta	aaa	gag	ctg	cgc	agc	att	ccg	cat	ctg	gaa	gtc	atc	aga	atc														
Ile	Leu	Lys	Glu	Leu	Arg	Ser	Ile	Pro	His	Leu	Glu	Val	Ile	Arg	Ile														
		195						200																					624
gga	aca	aga	gct	ccc	gtc	gtc	ttt	ccg	cag	cgc	att	acc	gat	cat	ctg														
Gly	Thr	Arg	Ala	Pro	Val	Val	Phe	Pro	Gln	Arg	Ile	Thr	Asp	His	Leu														672
		210						215																					
tgc	gag	ata	ttg	aaa	aaa	tat	cat	ccg	gtc	tgg	ctg	aac	acc	cat	ttt														
Cys	Glu	Ile	Leu	Lys	Lys	Tyr	His	Pro	Val	Trp	Leu	Asn	Thr	His	Phe														720
		225						230																					
aac	aca	agc	atc	gaa	atg	aca	gaa	gaa	tcc	gtt	gag	gca	tgt	gaa	aag														
Asn	Thr	Ser	Ile	Glu	Met	Thr	Glu	Glu	Ser	Val	Glu	Ala	Cys	Glu	Lys														768
				245					250																				
ctg	gtg	aac	gcg	gga	gtg	ccg	gtc	gga	aat	cag	gct	gtc	gta	tta	gca														
Leu	Val	Asn	Ala	Gly	Val	Pro	Val	Gly	Asn	Gln	Ala	Val	Val	Leu	Ala														816
				260					265																				
ggt	att	aat	gat	tcg	gtt	cca	att	atg	aaa	aag	ctc	atg	cat	gac	ttg														
Gly	Ile	Asn	Asp	Ser	Val	Pro	Ile	Met	Lys	Lys	Leu	Met	His	Asp	Leu														864
				275					280																				
gta	aaa	atc	aga	gtc	cgt	cct	tat	tat	att	tac	caa	tgt	gat	ctg	tca														
Val	Lys	Ile	Arg	Val	Arg	Pro	Tyr	Tyr	Ile	Tyr	Gln	Cys	Asp	Leu	Ser														912
				290					295																				
gaa	gga	ata	ggg	cat	ttc	aga	gct	cct	gtt	tcc	aaa	ggt	ttg	gag	atc														
Glu	Gly	Ile	Gly	His	Phe	Arg	Ala	Pro	Val	Ser	Lys	Gly	Leu	Glu	Ile														960
						310					315																		
att	gaa	ggg	ctg	aga	ggt	cat	acc	tca	ggc	tat	gcg	gtt	cct	acc	ttt														
Ile	Glu	Gly	Leu	Arg	Gly	His	Thr	Ser	Gly	Tyr	Ala	Val	Pro	Thr	Phe														1008
						325				330																			
gtc	gtt	cac	gca	cca	ggc	gga	gga	ggt	aaa	atc	gcc	ctg	cag	ccg	aac														
Val	Val	His	Ala	Pro	Gly	Gly	Gly	Gly	Lys	Ile	Ala	Leu	Gln	Pro	Asn														1056
						340				345																			
tat	gtc	ctg	tca	caa	agt	cct	gac	aaa	gtg	atc	tta	aga	aat	ttt	gaa														
Tyr	Val	Leu	Ser	Gln	Ser	Pro	Asp	Lys	Val	Ile	Leu	Arg	Asn	Phe	Glu														1104
						355				360																			
ggt	gtg	att	acg	tca	tat	ccg	gaa	cca	gag	aat	tat	atc	ccc	aat	cag														
Gly	Val	Ile	Thr	Ser	Tyr	Pro	Glu	Pro	Glu	Asn	Tyr	Ile	Pro	Asn	Gln														1152
						370				375																			
gca	gac	gcc	tat	ttt	gag	tcc	gtt	ttc	cct	gaa	acc	gct	gac	aaa	aag														
Ala	Asp	Ala	Tyr	Phe	Glu	Ser	Val	Phe	Pro	Glu	Thr	Ala	Asp	Lys	Lys														1200
						385				390																			
gag	ccg	atc	ggg	ctg	agt	gcc	att	ttt	gct	gac	aaa	gaa	gtt	tcg	ttt														
Glu	Pro	Ile	Gly	Leu	Ser	Ala	Ile	Phe	Ala	Asp	Lys	Glu	Val	Ser	Phe														1248
						405				410																			
aca	cct	gaa	aat	gta	gac	aga	atc	aaa	agg	aga	gag	gca	tac	atc	gca														
Thr	Pro	Glu	Asn	Val	Asp	Arg	Ile	Lys	Arg	Arg	Glu	Ala	Tyr	Ile	Ala														1296
						420				425																			

aat ccg gag cat gaa aca tta aaa gat cgg cgt gag aaa aga gat cag 1344  
 Asn Pro Glu His Glu Thr Leu Lys Asp Arg Arg Glu Lys Arg Asp Gln  
 435 440 445

ctc aaa gaa aag aaa ttt ttg gcg cag cag aaa aaa cag aaa gag act 1392  
 Leu Lys Glu Lys Lys Phe Leu Ala Gln Gln Lys Lys Gln Lys Glu Thr  
 450 455 460

gaa tgc gga ggg gat tct tca tga 1416  
 Glu Cys Gly Gly Asp Ser Ser  
 465 470

<210> 21  
 <211> 471  
 <212> PRT  
 <213> Bacillus subtilis

<400> 21

Met Lys Asn Lys Trp Tyr Lys Pro Lys Arg His Trp Lys Glu Ile Glu  
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Leu Trp Lys Asp Val Pro Glu Glu Lys Trp Asn Asp Trp Leu Trp Gln  
 20 25 30

Leu Thr His Thr Val Arg Thr Leu Asp Asp Leu Lys Lys Val Ile Asn  
 35 40 45

Leu Thr Glu Asp Glu Glu Glu Gly Val Arg Ile Ser Thr Lys Thr Ile  
 50 55 60

Pro Leu Asn Ile Thr Pro Tyr Tyr Ala Ser Leu Met Asp Pro Asp Asn  
 65 70 75 80

Pro Arg Cys Pro Val Arg Met Gln Ser Val Pro Leu Ser Glu Glu Met  
 85 90 95

His Lys Thr Lys Tyr Asp Met Glu Asp Pro Leu His Glu Asp Glu Asp  
 100 105 110

Ser Pro Val Pro Gly Leu Thr His Arg Tyr Pro Asp Arg Val Leu Phe  
 115 120 125

Leu Val Thr Asn Gln Cys Ser Val Tyr Cys Arg Tyr Cys Thr Arg Arg  
 130 135 140

Arg Phe Ser Gly Gln Ile Gly Met Gly Val Pro Lys Lys Gln Leu Asp  
 145 150 155 160



Ala Ala Ile Ala Tyr Ile Arg Glu Thr Pro Glu Ile Arg Asp Cys Leu  
 165 170 175

Ile Ser Gly Gly Asp Gly Leu Leu Ile Asn Asp Gln Ile Leu Glu Tyr  
 180 185 190

Ile Leu Lys Glu Leu Arg Ser Ile Pro His Leu Glu Val Ile Arg Ile  
 195 200 205

Gly Thr Arg Ala Pro Val Val Phe Pro Gln Arg Ile Thr Asp His Leu  
 210 215 220

Cys Glu Ile Leu Lys Lys Tyr His Pro Val Trp Leu Asn Thr His Phe  
 225 230 235 240

Asn Thr Ser Ile Glu Met Thr Glu Glu Ser Val Glu Ala Cys Glu Lys  
 245 250 255

Leu Val Asn Ala Gly Val Pro Val Gly Asn Gln Ala Val Val Leu Ala  
 260 265 270

Gly Ile Asn Asp Ser Val Pro Ile Met Lys Lys Leu Met His Asp Leu  
 275 280 285

Val Lys Ile Arg Val Arg Pro Tyr Tyr Ile Tyr Gln Cys Asp Leu Ser  
 290 295 300

Glu Gly Ile Gly His Phe Arg Ala Pro Val Ser Lys Gly Leu Glu Ile  
 305 310 315 320

Ile Glu Gly Leu Arg Gly His Thr Ser Gly Tyr Ala Val Pro Thr Phe  
 325 330 335

Val Val His Ala Pro Gly Gly Gly Gly Lys Ile Ala Leu Gln Pro Asn  
 340 345 350

Tyr Val Leu Ser Gln Ser Pro Asp Lys Val Ile Leu Arg Asn Phe Glu  
 355 360 365

Gly Val Ile Thr Ser Tyr Pro Glu Pro Glu Asn Tyr Ile Pro Asn Gln  
 370 375 380

Ala Asp Ala Tyr Phe Glu Ser Val Phe Pro Glu Thr Ala Asp Lys Lys  
 385 390 395 400

Glu Pro Ile Gly Leu Ser Ala Ile Phe Ala Asp Lys Glu Val Ser Phe

[illegible]

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<210> 22
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<213> Clostridium propionicum
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<220>
<221> CDS
<222> (1) .. (438)
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[illegible]

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Gln Arg Gly Pro Gln Glu Ser Ser Phe Lys Glu Arg Lys His Pro Gly			
130	135	140	

gaa tga	438
Glu	
145	

<210> 23  
 <211> 145  
 <212> PRT  
 <213> Clostridium propionicum

<400> 23

Met Val Gly Lys Lys Val Val His His Leu Met Met Ser Ala Lys Asp
1 5 10 15

Ala His Tyr Thr Gly Asn Leu Val Asn Gly Ala Arg Ile Val Asn Gln
20 25 30

Trp Gly Asp Val Gly Thr Glu Leu Met Val Tyr Val Asp Gly Asp Ile
35 40 45

Ser Leu Phe Leu Gly Tyr Lys Asp Ile Glu Phe Thr Ala Pro Val Tyr
50 55 60

Val Gly Asp Phe Met Glu Tyr His Gly Trp Ile Glu Lys Val Gly Asn
65 70 75 80

Gln Ser Tyr Thr Cys Lys Phe Glu Ala Trp Lys Val Ala Thr Met Val
85 90 95

Asp Ile Thr Asn Pro Gln Asp Thr Arg Ala Thr Ala Cys Glu Pro Pro
100 105 110

Val Leu Cys Gly Arg Ala Thr Gly Ser Leu Phe Ile Ala Lys Lys Asp
115 120 125

Gln Arg Gly Pro Gln Glu Ser Ser Phe Lys Glu Arg Lys His Pro Gly
130 135 140

Glu  
 145

<210> 24  
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&lt;213&gt; Megasphaera elsdenii

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (1554)

&lt;223&gt;

&lt;400&gt; 24

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Met Arg Lys Val Glu Ile Ile Thr Ala Glu Gln Ala Ala Gln Leu Val	
1 5 10 15	
aaa gac aac gac acg att acg tct atc ggc ttt gtc agc agc gcc cat	96
Lys Asp Asn Asp Thr Ile Thr Ser Ile Gly Phe Val Ser Ser Ala His	
20 25 30	
ccg gaa gca ctg acc aaa gct ttg gaa aaa cgg ttc ctg gac acg aac	144
Pro Glu Ala Leu Thr Lys Ala Leu Glu Lys Arg Phe Leu Asp Thr Asn	
35 40 45	
acc ccg cag aac ttg acc tac atc tat gca ggc tct cag ggc aaa cgc	192
Thr Pro Gln Asn Leu Thr Tyr Ile Tyr Ala Gly Ser Gln Gly Lys Arg	
50 55 60	
gat ggc cgt gcc gct gaa cat ctg gca cac aca ggc ctt ttg aaa cgc	240
Asp Gly Arg Ala Ala Glu His Leu Ala His Thr Gly Leu Leu Lys Arg	
65 70 75 80	
gcc atc atc ggt cac tgg cag act gta ccg gct atc ggt aaa ctg gct	288
Ala Ile Ile Gly His Trp Gln Thr Val Pro Ala Ile Gly Lys Leu Ala	
85 90 95	
gtc gaa aac aag att gaa gct tac aac ttc tcg cag ggc acg ttg gtc	336
Val Glu Asn Lys Ile Glu Ala Tyr Asn Phe Ser Gln Gly Thr Leu Val	
100 105 110	
cac tgg ttc cgc gcc ttg gca ggt cat aag ctc ggc gtc ttc acc gac	384
His Trp Phe Arg Ala Leu Ala Gly His Lys Leu Gly Val Phe Thr Asp	
115 120 125	
atc ggt ctg gaa act ttc ctc gat ccc cgt cag ctc ggc ggc aag ctc	432
Ile Gly Leu Glu Thr Phe Leu Asp Pro Arg Gln Leu Gly Gly Lys Leu	
130 135 140	
aat gac gta acc aaa gaa gac ctc gtc aaa ctg atc gaa gtc gat ggt	480
Asn Asp Val Thr Lys Glu Asp Leu Val Lys Leu Ile Glu Val Asp Gly	
145 150 155 160	
cat gaa cag ctt ttc tac ccg acc ttc ccg gtc aac gta gct ttc ctc	528
His Glu Gln Leu Phe Tyr Pro Thr Phe Pro Val Asn Val Ala Phe Leu	
165 170 175	
cgc ggt acg tat gct gat gaa tcc ggc aat atc acc atg gac gaa gaa	576
Arg Gly Thr Tyr Ala Asp Glu Ser Gly Asn Ile Thr Met Asp Glu Glu	
180 185 190	
atc ggg cct ttc gaa agc act tcc gta gcc cag gcc gtt cac aac tgt	624
Ile Gly Pro Phe Glu Ser Thr Ser Val Ala Gln Ala Val His Asn Cys	
195 200 205	

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ctc gac ccg cgc atg gtc aag atc cct ggc atc tat gtc gac tac gtc Leu Asp Pro Arg Met Val Lys Ile Pro Gly Ile Tyr Val Asp Tyr Val 225 230 235 240	720
gtc gta gca gct ccg gaa gac cat cag cag acg tat gac tgc gaa tac Val Val Ala Ala Pro Glu Asp His Gln Gln Thr Tyr Asp Cys Glu Tyr 245 250 255	768
gat ccg tcc ctc agc ggt gaa cat cgt gct cct gaa ggc gct acc gat Asp Pro Ser Leu Ser Gly Glu His Arg Ala Pro Glu Gly Ala Thr Asp 260 265 270	816
gca gct ctc ccc atg agc gct aag aaa atc atc ggc cgc cgc ggc gct Ala Ala Leu Pro Met Ser Ala Lys Lys Ile Ile Gly Arg Arg Gly Ala 275 280 285	864
ttg gaa ttg act gaa aac gct gtc gtc aac ctc ggc gtc ggt gct ccg Leu Glu Leu Thr Glu Asn Ala Val Val Asn Leu Gly Val Gly Ala Pro 290 295 300	912
gaa tac gtt gct tct gtt gcc ggt gaa gaa ggt atc gcc gat acc att Glu Tyr Val Ala Ser Val Ala Gly Glu Glu Gly Ile Ala Asp Thr Ile 305 310 315 320	960
acc ctg acc gtc gaa ggt ggc gcc atc ggt ggc gta ccg cag ggc ggt Thr Leu Thr Val Glu Gly Gly Ala Ile Gly Gly Val Pro Gln Gly Gly 325 330 335	1008
gcc cgc ttc ggt tcc tcc cgc aat gcc gat gcc atc atc gac cac acc Ala Arg Phe Gly Ser Ser Arg Asn Ala Asp Ala Ile Ile Asp His Thr 340 345 350	1056
tat cag ttc gac ttc tac gat ggc ggc ggt ctg gac atc gct tac ctc Tyr Gln Phe Asp Phe Tyr Asp Gly Gly Gly Leu Asp Ile Ala Tyr Leu 355 360 365	1104
ggc ctg gcc cag tgc gat ggc tcc ggc aac atc aac gtc agc aag ttc Gly Leu Ala Gln Cys Asp Gly Ser Gly Asn Ile Asn Val Ser Lys Phe 370 375 380	1152
ggt act aac gtt gcc ggc tgc ggc ggt ttc ccc aac att tcc cag cag Gly Thr Asn Val Ala Gly Cys Gly Gly Phe Pro Asn Ile Ser Gln Gln 385 390 395 400	1200
aca ccg aat gtt tac ttc tgc ggc acc ttc acg gct ggc ggc ttg aaa Thr Pro Asn Val Tyr Phe Cys Gly Thr Phe Thr Ala Gly Gly Leu Lys 405 410 415	1248
atc gct gtc gaa gac ggc aaa gtc aag atc ctc cag gaa ggc aaa gcc Ile Ala Val Glu Asp Gly Lys Val Lys Ile Leu Gln Glu Gly Lys Ala 420 425 430	1296
aag aag ttc atc aaa gct gtc gac cag atc act ttc aac ggt tcc tat Lys Lys Phe Ile Lys Ala Val Asp Gln Ile Thr Phe Asn Gly Ser Tyr 435 440 445	1344
gca gcc cgc aac ggc aaa cac gtt ctc tac atc aca gaa cgc tgc gta	1392

Ala Ala Arg Asn Gly Lys His Val Leu Tyr Ile Thr Glu Arg Cys Val  
 450 455 460

ttt gaa ctg acc aaa gaa ggc ttg aaa ctc atc gaa gtc gca ccg ggc 1440  
 Phe Glu Leu Thr Lys Glu Gly Leu Lys Leu Ile Glu Val Ala Pro Gly  
 465 470 475 480

atc gat att gaa aaa gat atc ctc gct cac atg gac ttc aag ccg atc 1488  
 Ile Asp Ile Glu Lys Asp Ile Leu Ala His Met Asp Phe Lys Pro Ile  
 485 490 495

att gat aat ccg aaa ctc atg gat gcc cgc ctc ttc cag gac ggt ccc 1536  
 Ile Asp Asn Pro Lys Leu Met Asp Ala Arg Leu Phe Gln Asp Gly Pro  
 500 505 510

atg gga ctg aaa aaa taa 1554  
 Met Gly Leu Lys Lys  
 515

<210> 25  
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 <212> PRT  
 <213> Megasphaera elsdenii

<400> 25

Met Arg Lys Val Glu Ile Ile Thr Ala Glu Gln Ala Ala Gln Leu Val  
 1 5 10 15

Lys Asp Asn Asp Thr Ile Thr Ser Ile Gly Phe Val Ser Ser Ala His  
 20 25 30

Pro Glu Ala Leu Thr Lys Ala Leu Glu Lys Arg Phe Leu Asp Thr Asn  
 35 40 45

Thr Pro Gln Asn Leu Thr Tyr Ile Tyr Ala Gly Ser Gln Gly Lys Arg  
 50 55 60

Asp Gly Arg Ala Ala Glu His Leu Ala His Thr Gly Leu Leu Lys Arg  
 65 70 75 80

Ala Ile Ile Gly His Trp Gln Thr Val Pro Ala Ile Gly Lys Leu Ala  
 85 90 95

Val Glu Asn Lys Ile Glu Ala Tyr Asn Phe Ser Gln Gly Thr Leu Val  
 100 105 110

His Trp Phe Arg Ala Leu Ala Gly His Lys Leu Gly Val Phe Thr Asp  
 115 120 125

Ile Gly Leu Glu Thr Phe Leu Asp Pro Arg Gln Leu Gly Gly Lys Leu  
 130 135 140

Asn Asp Val Thr Lys Glu Asp Leu Val Lys Leu Ile Glu Val Asp Gly  
 145 150 155 160

His Glu Gln Leu Phe Tyr Pro Thr Phe Pro Val Asn Val Ala Phe Leu  
 165 170 175

Arg Gly Thr Tyr Ala Asp Glu Ser Gly Asn Ile Thr Met Asp Glu Glu  
 180 185 190

Ile Gly Pro Phe Glu Ser Thr Ser Val Ala Gln Ala Val His Asn Cys  
 195 200 205

Gly Gly Lys Val Val Val Gln Val Lys Asp Val Val Ala His Gly Ser  
 210 215 220

Leu Asp Pro Arg Met Val Lys Ile Pro Gly Ile Tyr Val Asp Tyr Val  
 225 230 235 240

Val Val Ala Ala Pro Glu Asp His Gln Gln Thr Tyr Asp Cys Glu Tyr  
 245 250 255

Asp Pro Ser Leu Ser Gly Glu His Arg Ala Pro Glu Gly Ala Thr Asp  
 260 265 270

Ala Ala Leu Pro Met Ser Ala Lys Lys Ile Ile Gly Arg Arg Gly Ala  
 275 280 285

Leu Glu Leu Thr Glu Asn Ala Val Val Asn Leu Gly Val Gly Ala Pro  
 290 295 300

Glu Tyr Val Ala Ser Val Ala Gly Glu Glu Gly Ile Ala Asp Thr Ile  
 305 310 315 320

Thr Leu Thr Val Glu Gly Gly Ala Ile Gly Gly Val Pro Gln Gly Gly  
 325 330 335

Ala Arg Phe Gly Ser Ser Arg Asn Ala Asp Ala Ile Ile Asp His Thr  
 340 345 350

Tyr Gln Phe Asp Phe Tyr Asp Gly Gly Gly Leu Asp Ile Ala Tyr Leu  
 355 360 365

Gly Leu Ala Gln Cys Asp Gly Ser Gly Asn Ile Asn Val Ser Lys Phe  
 370 375 380

Gly Thr Asn Val Ala Gly Cys Gly Gly Phe Pro Asn Ile Ser Gln Gln  
385 390 395 400

Thr Pro Asn Val Tyr Phe Cys Gly Thr Phe Thr Ala Gly Gly Leu Lys  
405 410 415

Ile Ala Val Glu Asp Gly Lys Val Lys Ile Leu Gln Glu Gly Lys Ala  
420 425 430

Lys Lys Phe Ile Lys Ala Val Asp Gln Ile Thr Phe Asn Gly Ser Tyr  
435 440 445

Ala Ala Arg Asn Gly Lys His Val Leu Tyr Ile Thr Glu Arg Cys Val  
450 455 460

Phe Glu Leu Thr Lys Glu Gly Leu Lys Leu Ile Glu Val Ala Pro Gly  
465 470 475 480

Ile Asp Ile Glu Lys Asp Ile Leu Ala His Met Asp Phe Lys Pro Ile  
485 490 495

Ile Asp Asn Pro Lys Leu Met Asp Ala Arg Leu Phe Gln Asp Gly Pro  
500 505 510

Met Gly Leu Lys Lys  
515

<210> 26  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 26  
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26

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<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 27  
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27



<210> 28  
 <211> 416  
 <212> PRT  
 <213> Porphyromonas gingivalis

<400> 28

Met Ala Glu Ser Arg Arg Lys Tyr Tyr Phe Pro Asp Val Thr Asp Glu  
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Gln Trp Asn Asp Trp His Trp Gln Val Leu Asn Arg Ile Glu Thr Leu  
 20 25 30

Asp Gln Leu Lys Lys Tyr Val Thr Leu Thr Ala Glu Glu Glu Gly  
 35 40 45

Val Lys Glu Ser Leu Lys Val Leu Arg Met Ala Ile Thr Pro Tyr Tyr  
 50 55 60

Leu Ser Leu Ile Asp Pro Glu Asn Pro Asn Cys Pro Ile Arg Lys Gln  
 65 70 75 80

Ala Ile Pro Thr His Gln Glu Leu Val Arg Ala Pro Glu Asp Gln Val  
 85 90 95

Asp Pro Leu Ser Glu Asp Glu Asp Ser Pro Val Pro Gly Leu Thr His  
 100 105 110

Arg Tyr Pro Asp Arg Val Leu Phe Leu Ile Thr Asp Lys Cys Ser Met  
 115 120 125

Tyr Cys Arg His Cys Thr Arg Arg Arg Phe Ala Gly Gln Lys Asp Ala  
 130 135 140

Ser Ser Pro Ser Glu Arg Ile Asp Arg Cys Ile Asp Tyr Ile Ala Asn  
 145 150 155 160

Thr Pro Thr Val Arg Asp Val Leu Leu Ser Gly Gly Asp Ala Leu Leu  
 165 170 175

Val Ser Asp Glu Arg Leu Glu Tyr Ile Leu Lys Arg Leu Arg Glu Ile  
 180 185 190

Pro His Val Glu Ile Val Arg Ile Gly Ser Arg Thr Pro Val Val Leu  
 195 200 205

Pro Gln Arg Ile Thr Pro Gln Leu Val Asp Met Leu Lys Lys Tyr His  
 210 215 220

Pro Val Trp Leu Asn Thr His Phe Asn His Pro Asn Glu Val Thr Glu  
225 230 235 240

Glu Ala Val Glu Ala Cys Glu Arg Met Ala Asn Ala Gly Ile Pro Leu  
245 250 255

Gly Asn Gln Thr Val Leu Leu Arg Gly Ile Asn Asp Cys Thr His Val  
260 265 270

Met Lys Arg Leu Val His Leu Leu Val Lys Met Arg Val Arg Pro Tyr  
275 280 285

Tyr Ile Tyr Val Cys Asp Leu Ser Leu Gly Ile Gly His Phe Arg Thr  
290 295 300

Pro Val Ser Lys Gly Ile Glu Ile Ile Glu Asn Leu Arg Gly His Thr  
305 310 315 320

Ser Gly Tyr Ala Val Pro Thr Phe Val Val Asp Ala Pro Gly Gly Gly  
325 330 335

Gly Lys Ile Pro Val Met Pro Asn Tyr Val Val Ser Gln Ser Pro Arg  
340 345 350

His Val Val Leu Arg Asn Tyr Glu Gly Val Ile Thr Thr Tyr Thr Glu  
355 360 365

Pro Glu Asn Tyr His Glu Glu Cys Asp Cys Glu Asp Cys Arg Ala Gly  
370 375 380

Lys His Lys Glu Gly Val Ala Ala Leu Ser Gly Gly Gln Gln Leu Ala  
385 390 395 400

Ile Glu Pro Ser Asp Leu Ala Arg Lys Lys Arg Lys Phe Asp Lys Asn  
405 410 415

<210> 29  
<211> 1251  
<212> DNA  
<213> Porphyromonas gingivalis

<220>  
<221> CDS  
<222> (1) .. (1251)  
<223>

<400> 29																	
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Met Ala Glu Ser Arg Arg Lys Tyr Tyr Phe Pro Asp Val Thr Asp Glu																	
1 5 10 15																	
caa tgg tac gac tgg cat tgg cag gtc ctc aat cga att gag acg ctc																	96
Gln Trp Tyr Asp Trp His Trp Gln Val Leu Asn Arg Ile Glu Thr Leu																	
20 25 30																	
gac cag ctg aaa aag tac gtt aca ctc acc gct gaa gaa gaa gag gga																	144
Asp Gln Leu Lys Lys Tyr Val Thr Leu Thr Ala Glu Glu Glu Glu Gly																	
35 40 45																	
gta aaa gaa tcg ccc aaa gta ctc cga atg gct atc aca cct tat tat																	192
Val Lys Glu Ser Pro Lys Val Leu Arg Met Ala Ile Thr Pro Tyr Tyr																	
50 55 60																	
ttg agt ttg ata gac ccc gag aat cct aat tgt ccg att cgt aaa caa																	240
Leu Ser Leu Ile Asp Pro Glu Asn Pro Asn Cys Pro Ile Arg Lys Gln																	
65 70 75 80																	
gcc att cct act caa cag gaa ctg gta cgt gct cct gaa gat cag gta																	288
Ala Ile Pro Thr Gln Gln Glu Leu Val Arg Ala Pro Glu Asp Gln Val																	
85 90 95																	
gac cca ctt agt gaa gat gaa gat tcg ccc gta ccc gga ctg act cat																	336
Asp Pro Leu Ser Glu Asp Glu Asp Ser Pro Val Pro Gly Leu Thr His																	
100 105 110																	
cgt tat ccg gat cgt gta ttg ttc ctt atc acg gac aaa tgt tcg atg																	384
Arg Tyr Pro Asp Arg Val Leu Phe Leu Ile Thr Asp Lys Cys Ser Met																	
115 120 125																	
tac tgt cgt cat tgt act cgc cgt cgc ttc gca gga cag aaa gat gct																	432
Tyr Cys Arg His Cys Thr Arg Arg Arg Phe Ala Gly Gln Lys Asp Ala																	
130 135 140																	
tct tct cct tct gag cgc atc gat cga tgc att gac tat ata gcc aat																	480
Ser Ser Pro Ser Glu Arg Ile Asp Arg Cys Ile Asp Tyr Ile Ala Asn																	
145 150 155 160																	
aca ccg aca gtc cgc gat gtt ttg cta tcg gga ggc gat gcc ctc ctt																	528
Thr Pro Thr Val Arg Asp Val Leu Leu Ser Gly Gly Asp Ala Leu Leu																	
165 170 175																	
gtc agc gac gaa cgc ttg gaa tac ata ttg aag cgt ctg cgc gaa ata																	576
Val Ser Asp Glu Arg Leu Glu Tyr Ile Leu Lys Arg Leu Arg Glu Ile																	
180 185 190																	
cct cat gtg gag att gtt cgt ata gga agc cgt acg ccg gta gtc ctc																	624
Pro His Val Glu Ile Val Arg Ile Gly Ser Arg Thr Pro Val Val Leu																	
195 200 205																	
cct cag cgt ata acg cct caa ttg gtg gat atg ctc aaa aaa tat cat																	672
Pro Gln Arg Ile Thr Pro Gln Leu Val Asp Met Leu Lys Lys Tyr His																	
210 215 220																	
ccg gtg tgg ctg aac act cac ttc aac cac ccg aat gaa gtt acc gaa																	720
Pro Val Trp Leu Asn Thr His Phe Asn His Pro Asn Glu Val Thr Glu																	
225 230 235 240																	

gaa gca gta gag gct tgt gaa aga atg gcc aat gcc ggt att ccg ttg 768  
 Glu Ala Val Glu Ala Cys Glu Arg Met Ala Asn Ala Gly Ile Pro Leu  
 245 250 255

ggt aac caa acg gtt tta ttg cgt gga atc aat gat tgt aca cat gtg 816  
 Gly Asn Gln Thr Val Leu Leu Arg Gly Ile Asn Asp Cys Thr His Val  
 260 265 270

atg aag aga ttg gta cat ttg ctg gta aag atg cgt gtg cgt cct tac 864  
 Met Lys Arg Leu Val His Leu Leu Val Lys Met Arg Val Arg Pro Tyr  
 275 280 285

tat ata tat gta tgc gat ctt tcg ctt gga ata ggt cat ttc cgc acg 912  
 Tyr Ile Tyr Val Cys Asp Leu Ser Leu Gly Ile Gly His Phe Arg Thr  
 290 295 300

ccg gta tct aaa gga atc gaa att atc gaa aat ttg cgc gga cac acc 960  
 Pro Val Ser Lys Gly Ile Glu Ile Ile Glu Asn Leu Arg Gly His Thr  
 305 310 315 320

tcg ggc tat gca gtt cct acc ttt gtg gta ggt gct ccg ggg ggt ggt 1008  
 Ser Gly Tyr Ala Val Pro Thr Phe Val Val Gly Ala Pro Gly Gly Gly  
 325 330 335

ggt aag ata cct gta acg ccg aac tat gtt gta tct cag tcc cca cga 1056  
 Gly Lys Ile Pro Val Thr Pro Asn Tyr Val Val Ser Gln Ser Pro Arg  
 340 345 350

cat gtg gtt ctt cgc aat tat gaa ggt gtt atc aca acc tat acg gag 1104  
 His Val Val Leu Arg Asn Tyr Glu Gly Val Ile Thr Thr Tyr Thr Glu  
 355 360 365

ccg gag aat tat cat gag gag tgc gat tgt gag gac tgt cga gcc ggt 1152  
 Pro Glu Asn Tyr His Glu Glu Cys Asp Cys Glu Asp Cys Arg Ala Gly  
 370 375 380

aag cat aaa gag ggt gta gct gca ctt tcc gga ggt cag cag ttg gct 1200  
 Lys His Lys Glu Gly Val Ala Ala Leu Ser Gly Gly Gln Gln Leu Ala  
 385 390 395 400

atc gag cct tcc gac tta gct cgc aaa aaa cgc aag ttt gat aag aac 1248  
 Ile Glu Pro Ser Asp Leu Ala Arg Lys Lys Arg Lys Phe Asp Lys Asn  
 405 410 415

tga 1251

&lt;210&gt; 30

&lt;211&gt; 416

&lt;212&gt; PRT

&lt;213&gt; Porphyromonas gingivalis

&lt;400&gt; 30

Met Ala Glu Ser Arg Arg Lys Tyr Tyr Phe Pro Asp Val Thr Asp Glu  
1 5 10 15

Gln Trp Tyr Asp Trp His Trp Gln Val Leu Asn Arg Ile Glu Thr Leu  
20 25 30

Asp Gln Leu Lys Lys Tyr Val Thr Leu Thr Ala Glu Glu Glu Glu Gly  
 35 40 45

Val Lys Glu Ser Pro Lys Val Leu Arg Met Ala Ile Thr Pro Tyr Tyr  
 50 55 60

Leu Ser Leu Ile Asp Pro Glu Asn Pro Asn Cys Pro Ile Arg Lys Gln  
 65 70 75 80

Ala Ile Pro Thr Gln Gln Glu Leu Val Arg Ala Pro Glu Asp Gln Val  
 85 90 95

Asp Pro Leu Ser Glu Asp Glu Asp Ser Pro Val Pro Gly Leu Thr His  
 100 105 110

Arg Tyr Pro Asp Arg Val Leu Phe Leu Ile Thr Asp Lys Cys Ser Met  
 115 120 125

Tyr Cys Arg His Cys Thr Arg Arg Arg Phe Ala Gly Gln Lys Asp Ala  
 130 135 140

Ser Ser Pro Ser Glu Arg Ile Asp Arg Cys Ile Asp Tyr Ile Ala Asn  
 145 150 155 160

Thr Pro Thr Val Arg Asp Val Leu Leu Ser Gly Gly Asp Ala Leu Leu  
 165 170 175

Val Ser Asp Glu Arg Leu Glu Tyr Ile Leu Lys Arg Leu Arg Glu Ile  
 180 185 190

Pro His Val Glu Ile Val Arg Ile Gly Ser Arg Thr Pro Val Val Leu  
 195 200 205

Pro Gln Arg Ile Thr Pro Gln Leu Val Asp Met Leu Lys Lys Tyr His  
 210 215 220

Pro Val Trp Leu Asn Thr His Phe Asn His Pro Asn Glu Val Thr Glu  
 225 230 235 240

Glu Ala Val Glu Ala Cys Glu Arg Met Ala Asn Ala Gly Ile Pro Leu  
 245 250 255

Gly Asn Gln Thr Val Leu Leu Arg Gly Ile Asn Asp Cys Thr His Val  
 260 265 270

Met Lys Arg Leu Val His Leu Leu Val Lys Met Arg Val Arg Pro Tyr  
 275 280 285

Tyr Ile Tyr Val Cys Asp Leu Ser Leu Gly Ile Gly His Phe Arg Thr  
 290 295 300

Pro Val Ser Lys Gly Ile Glu Ile Ile Glu Asn Leu Arg Gly His Thr  
 305 310 315 320

Ser Gly Tyr Ala Val Pro Thr Phe Val Val Gly Ala Pro Gly Gly Gly  
 325 330 335

Gly Lys Ile Pro Val Thr Pro Asn Tyr Val Val Ser Gln Ser Pro Arg  
 340 345 350

His Val Val Leu Arg Asn Tyr Glu Gly Val Ile Thr Thr Tyr Thr Glu  
 355 360 365

Pro Glu Asn Tyr His Glu Glu Cys Asp Cys Glu Asp Cys Arg Ala Gly  
 370 375 380

Lys His Lys Glu Gly Val Ala Ala Leu Ser Gly Gly Gln Gln Leu Ala  
 385 390 395 400

Ile Glu Pro Ser Asp Leu Ala Arg Lys Lys Arg Lys Phe Asp Lys Asn  
 405 410 415

<210> 31  
 <211> 471  
 <212> PRT  
 <213> Bacillus subtilis

<400> 31

Met Lys Asn Lys Trp Tyr Lys Pro Lys Arg His Trp Lys Glu Ile Glu  
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Leu Trp Lys Asp Val Pro Glu Glu Lys Trp Asn Asp Trp Leu Trp Gln  
 20 25 30

Leu Thr His Thr Val Arg Thr Leu Asp Asp Leu Lys Lys Val Ile Asn  
 35 40 45

Leu Thr Glu Asp Glu Glu Glu Gly Val Arg Ile Ser Thr Lys Thr Ile  
 50 55 60

Pro Leu Asn Ile Thr Pro Tyr Tyr Ala Ser Leu Met Asp Pro Asp Asn  
 65 70 75 80

Pro Arg Cys Pro Val Arg Met Gln Ser Val Pro Leu Ser Glu Glu Met  
                     85                    90                    95

His Lys Thr Lys Tyr Asp Leu Glu Asp Pro Leu His Glu Asp Glu Asp  
                     100                    105                    110

Ser Pro Val Pro Gly Leu Thr His Arg Tyr Pro Asp Arg Val Leu Phe  
                     115                    120                    125

Leu Val Thr Asn Gln Cys Ser Met Tyr Cys Arg Tyr Cys Thr Arg Arg  
                     130                    135                    140

Arg Phe Ser Gly Gln Ile Gly Met Gly Val Pro Lys Lys Gln Leu Asp  
                     145                    150                    155                    160

Ala Ala Ile Ala Tyr Ile Arg Glu Thr Pro Glu Ile Arg Asp Cys Leu  
                     165                    170                    175

Ile Ser Gly Gly Asp Gly Leu Leu Ile Asn Asp Gln Ile Leu Glu Tyr  
                     180                    185                    190

Ile Leu Lys Glu Leu Arg Ser Ile Pro His Leu Glu Val Ile Arg Ile  
                     195                    200                    205

Gly Thr Arg Ala Pro Val Val Phe Pro Gln Arg Ile Thr Asp His Leu  
                     210                    215                    220

Cys Glu Ile Leu Lys Lys Tyr His Pro Val Trp Leu Asn Thr His Phe  
                     225                    230                    235                    240

Asn Thr Ser Ile Glu Met Thr Glu Glu Ser Val Glu Ala Cys Glu Lys  
                     245                    250                    255

Leu Val Asn Ala Gly Val Pro Val Gly Asn Gln Ala Val Val Leu Ala  
                     260                    265                    270

Gly Ile Asn Asp Ser Val Pro Ile Met Lys Lys Leu Met His Asp Leu  
                     275                    280                    285

Val Lys Ile Arg Val Arg Pro Tyr Tyr Ile Tyr Gln Cys Asp Leu Ser  
                     290                    295                    300

Glu Gly Ile Gly His Phe Arg Ala Pro Val Ser Lys Gly Leu Glu Ile  
                     305                    310                    315                    320

Ile Glu Gly Leu Arg Gly His Thr Ser Gly Tyr Ala Val Pro Thr Phe  
                   325                                  330                                  335

Val Val Asp Ala Pro Gly Gly Gly Gly Lys Ile Ala Leu Gln Pro Asn  
                   340                                  345                                  350

Tyr Val Leu Ser Gln Ser Pro Asp Lys Val Ile Leu Arg Asn Phe Glu  
                   355                                  360                                  365

Gly Val Ile Thr Ser Tyr Pro Glu Pro Glu Asn Tyr Ile Pro Asn Gln  
                   370                                  375                                  380

Ala Asp Ala Tyr Phe Glu Ser Val Phe Pro Glu Thr Ala Asp Lys Lys  
                   385                                  390                                  395                                  400

Glu Pro Ile Gly Leu Ser Ala Ile Phe Ala Asp Lys Glu Val Ser Phe  
                                   405                                  410                                  415

Thr Pro Glu Asn Val Asp Arg Ile Lys Arg Arg Glu Ala Tyr Ile Ala  
                   420                                  425                                  430

Asn Pro Glu His Glu Thr Leu Lys Asp Arg Arg Glu Lys Arg Asp Gln  
                   435                                  440                                  445

Leu Lys Glu Lys Lys Phe Leu Ala Gln Gln Lys Lys Gln Lys Glu Thr  
                   450                                  455                                  460

Glu Cys Gly Gly Asp Ser Ser  
                   465                                  470

<210> 32

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 32

cgcattcaag tcaaagacgt tcaggcta

28

<210> 33

<211> 1387

<212> DNA

<213> *Alcaligenes faecalis*

<220>

<221> CDS

<222> (408) .. (1304)



&lt;223&gt;

&lt;400&gt; 33

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gcaaacccttc gccaaagggtg cgcctgggttc ggctcgtttg tcctttgagc tgctggagag	120
ggtgcatcac ctgtcttttg cccgatgtttt ccgtctggaa tacatttgtgt cgctgcaatg	180
tggcgctacag ggcgacttcc aggaaggcat acgggcactg ctgattgata aagacaaaca	240
gccgcgctgg aatcctgcct cgctggaaca ggccgatgca cgctgggtgg aacgtttttt	300
tgttcctgcc tggccggcag aaacgactca tcccttggtt gacctgtaac ccaggcagac	360
cgctgcggcg ccagacggcg ccgctttcat aatgacgagg agacaaa atg agt aac	416
	Met Ser Asn
	1
acg att gca ttt atc ggg ctg ggc cat atg ggt aaa ccc atg gcg ctg	464
Thr Ile Ala Phe Ile Gly Leu Gly His Met Gly Lys Pro Met Ala Leu	
5 10 15	
aat ctg ctc aaa gcc ggt cat agc ctg aac gtc ttt gac ttg aat gcg	512
Asn Leu Leu Lys Ala Gly His Ser Leu Asn Val Phe Asp Leu Asn Ala	
20 25 30 35	
caa gcc atg cag gaa ctg cag gca gca ggg gca cag gtg ggg gaa tcg	560
Gln Ala Met Gln Glu Leu Gln Ala Ala Gly Ala Gln Val Gly Glu Ser	
40 45 50	
gcg gtg caa atc gcc caa gac gcg cag atg gtc ttt acc atg ctg cct	608
Ala Val Gln Ile Ala Gln Asp Ala Gln Met Val Phe Thr Met Leu Pro	
55 60 65	
gct ggc cgc cat gtt cgt cag gtt tac gag ggc gag aac ggc ttg ctg	656
Ala Gly Arg His Val Arg Gln Val Tyr Glu Gly Glu Asn Gly Leu Leu	
70 75 80	
cag act gtg gcc ccc ggt acg gtg ctg gtc gat tgc agc acc att gat	704
Gln Thr Val Ala Pro Gly Thr Val Leu Val Asp Cys Ser Thr Ile Asp	
85 90 95	
gcg caa acc agc cag gat ctg gcg gcc aaa gcc agc aag ctg ggt ctg	752
Ala Gln Thr Ser Gln Asp Leu Ala Ala Lys Ala Ser Lys Leu Gly Leu	
100 105 110 115	
ttc atg ctg gat gcg ccg gtc tcc ggt ggg acc ggt ggc gcc att gct	800
Phe Met Leu Asp Ala Pro Val Ser Gly Gly Thr Gly Gly Ala Ile Ala	
120 125 130	
ggc acc ttg acc ttt atg gtc ggg ggc gag gat cag gcc ctg gaa aag	848
Gly Thr Leu Thr Phe Met Val Gly Gly Glu Asp Gln Ala Leu Glu Lys	
135 140 145	
gcg cgc cct tac ttg gat gcc atg ggc aag aac att ttc cac gcg ggt	896
Ala Arg Pro Tyr Leu Asp Ala Met Gly Lys Asn Ile Phe His Ala Gly	
150 155 160	
aaa gcc ggt gcg ggt cag gtt gcc aag att tgc aac aat atg ctc ttg	944

Lys Ala Gly Ala Gly Gln Val Ala Lys Ile Cys Asn Asn Met Leu Leu  
 165 170 175  
 ggg att ttg atg gcg ggt act gct gaa gcc ttg gct ttg ggc gtt gcc 992  
 Gly Ile Leu Met Ala Gly Thr Ala Glu Ala Leu Ala Leu Gly Val Ala  
 180 185 190 195  
 cac ggt ctg gac cct gcc gtg ctg tcg acc atc atg gcg cgc agt tcc 1040  
 His Gly Leu Asp Pro Ala Val Leu Ser Thr Ile Met Ala Arg Ser Ser  
 200 205 210  
 ggt cga aac tgg gca acc gag ctg tac aac ccc tgg cct ggg gtg atg 1088  
 Gly Arg Asn Trp Ala Thr Glu Leu Tyr Asn Pro Trp Pro Gly Val Met  
 215 220 225  
 ccg gat gta ccg gct tcg cgt gat tat cag ggc ggt ttt gcg acg ggc 1136  
 Pro Asp Val Pro Ala Ser Arg Asp Tyr Gln Gly Gly Phe Ala Thr Gly  
 230 235 240  
 ctg atg ctc aaa gac ctg ggt ctg gca gcc gat gcg gct gtc agc cag 1184  
 Leu Met Leu Lys Asp Leu Gly Leu Ala Ala Asp Ala Ala Val Ser Gln  
 245 250 255  
 aac agc gcg acg cct ttg ggc gaa ctg gca cgt aac ctg ttc gcc ttg 1232  
 Asn Ser Ala Thr Pro Leu Gly Glu Leu Ala Arg Asn Leu Phe Ala Leu  
 260 265 270 275  
 cac gcc gca caa ggt cag aat gca ggg ctg gat ttc tcc agc att ctt 1280  
 His Ala Ala Gln Gly Gln Asn Ala Gly Leu Asp Phe Ser Ser Ile Leu  
 280 285 290  
 aat ttg tac cgt cag aag cac taa gttctggcag tgcgtagggc aggggctgca 1334  
 Asn Leu Tyr Arg Gln Lys His  
 295  
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 <211> 298  
 <212> PRT  
 <213> *Alcaligenes faecalis*  
  
 <400> 34  
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 Met Ala Leu Asn Leu Leu Lys Ala Gly His Ser Leu Asn Val Phe Asp  
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 Leu Asn Ala Gln Ala Met Gln Glu Leu Gln Ala Ala Gly Ala Gln Val  
 35 40 45  
 Gly Glu Ser Ala Val Gln Ile Ala Gln Asp Ala Gln Met Val Phe Thr  
 50 55 60

Met Leu Pro Ala Gly Arg His Val Arg Gln Val Tyr Glu Gly Glu Asn  
65 70 75 80

Gly Leu Leu Gln Thr Val Ala Pro Gly Thr Val Leu Val Asp Cys Ser  
85 90 95

Thr Ile Asp Ala Gln Thr Ser Gln Asp Leu Ala Ala Lys Ala Ser Lys  
100 105 110

Leu Gly Leu Phe Met Leu Asp Ala Pro Val Ser Gly Gly Thr Gly Gly  
115 120 125

Ala Ile Ala Gly Thr Leu Thr Phe Met Val Gly Gly Glu Asp Gln Ala  
130 135 140

Leu Glu Lys Ala Arg Pro Tyr Leu Asp Ala Met Gly Lys Asn Ile Phe  
145 150 155 160

His Ala Gly Lys Ala Gly Ala Gly Gln Val Ala Lys Ile Cys Asn Asn  
165 170 175

Met Leu Leu Gly Ile Leu Met Ala Gly Thr Ala Glu Ala Leu Ala Leu  
180 185 190

Gly Val Ala His Gly Leu Asp Pro Ala Val Leu Ser Thr Ile Met Ala  
195 200 205

Arg Ser Ser Gly Arg Asn Trp Ala Thr Glu Leu Tyr Asn Pro Trp Pro  
210 215 220

Gly Val Met Pro Asp Val Pro Ala Ser Arg Asp Tyr Gln Gly Gly Phe  
225 230 235 240

Ala Thr Gly Leu Met Leu Lys Asp Leu Gly Leu Ala Ala Asp Ala Ala  
245 250 255

Val Ser Gln Asn Ser Ala Thr Pro Leu Gly Glu Leu Ala Arg Asn Leu  
260 265 270

Phe Ala Leu His Ala Ala Gln Gly Gln Asn Ala Gly Leu Asp Phe Ser  
275 280 285

Ser Ile Leu Asn Leu Tyr Arg Gln Lys His  
290 295

<210> 35

<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 35  
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36

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34

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36

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28

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35

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acgttgatct ccttctacat tattttttca gtcccatg 38  
  
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catgggactg aaaaaataat gtagaaggag atcaacgt 38  
  
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32

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53

<210> 47

<211> 30

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<220>

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<400> 47

ctagtctaga ggaaaccgct taacgaactc

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<210> 48

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<212> DNA

<213> Artificial Sequence

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<223> PCR primer

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gggaattcca tatgcgtaac ttctctctgc tattattgag ggtgctttgc atcc

54

<210> 49

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<212> DNA

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<223> PCR primer

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31

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<212> DNA

<213> Artificial Sequence

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39

&lt;210&gt; 51

&lt;211&gt; 39

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; PCR primer

&lt;400&gt; 51

gctataagaa tagcgattta agctgaaagg gagacggac

39

&lt;210&gt; 52

&lt;211&gt; 30

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; PCR primer

&lt;400&gt; 52

cgacggatcc gcagtgagtg agccttggag

30

&lt;210&gt; 53

&lt;211&gt; 435

&lt;212&gt; DNA

&lt;213&gt; Clostridium propionicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (435)

&lt;223&gt;

&lt;400&gt; 53

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Met	Val	Gly	Lys	Lys	Val	Val	His	His	Leu	Met	Met	Ser	Ala	Lys	Asp	
1				5					10					15		

gct	cac	tat	act	gga	aac	tta	gta	aac	ggc	gct	aga	atc	gtg	aat	cag	96
Ala	His	Tyr	Thr	Gly	Asn	Leu	Val	Asn	Gly	Ala	Arg	Ile	Val	Asn	Gln	
			20					25					30			

tgg	ggc	gac	gta	ggt	aca	gaa	tta	atg	ggt	tat	ggt	gat	ggg	gac	atc	144
Trp	Gly	Asp	Val	Gly	Thr	Glu	Leu	Met	Val	Tyr	Val	Asp	Gly	Asp	Ile	
		35					40					45				

agc	tta	ttc	ttg	ggc	tac	aaa	gat	atc	gaa	ttc	aca	gct	cct	gta	tat	192
Ser	Leu	Phe	Leu	Gly	Tyr	Lys	Asp	Ile	Glu	Phe	Thr	Ala	Pro	Val	Tyr	
		50				55					60					

ggt	ggt	gat	ttt	atg	gaa	tac	cac	ggc	tgg	att	gaa	aaa	ggt	ggc	aac	240
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Val Gly Asp Phe Met Glu Tyr His Gly Trp Ile Glu Lys Val Gly Asn  
65 70 75 80

cag tcc tat aca tgt aaa ttt gaa gca tgg aaa gta gca aag atg gtt 288  
Gln Ser Tyr Thr Cys Lys Phe Glu Ala Trp Lys Val Ala Lys Met Val  
85 90 95

gat atc aca aat cca cag gat aca cgt gca aca gct tgt gaa cct ccg 336  
Asp Ile Thr Asn Pro Gln Asp Thr Arg Ala Thr Ala Cys Glu Pro Pro  
100 105 110

gta ctt tgt ggt act gca aca ggc agc ctt ttc atc gca aag gat aat 384  
Val Leu Cys Gly Thr Ala Thr Gly Ser Leu Phe Ile Ala Lys Asp Asn  
115 120 125

cag aga ggt cct cag gaa tct tcc ttc aag gat gca aag cac cct caa 432  
Gln Arg Gly Pro Gln Glu Ser Ser Phe Lys Asp Ala Lys His Pro Gln  
130 135 140

taa 435

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Met Val Gly Lys Lys Val Val His His Leu Met Met Ser Ala Lys Asp  
1 5 10 15

Ala His Tyr Thr Gly Asn Leu Val Asn Gly Ala Arg Ile Val Asn Gln  
20 25 30

Trp Gly Asp Val Gly Thr Glu Leu Met Val Tyr Val Asp Gly Asp Ile  
35 40 45

Ser Leu Phe Leu Gly Tyr Lys Asp Ile Glu Phe Thr Ala Pro Val Tyr  
50 55 60

Val Gly Asp Phe Met Glu Tyr His Gly Trp Ile Glu Lys Val Gly Asn  
65 70 75 80

Gln Ser Tyr Thr Cys Lys Phe Glu Ala Trp Lys Val Ala Lys Met Val  
85 90 95

Asp Ile Thr Asn Pro Gln Asp Thr Arg Ala Thr Ala Cys Glu Pro Pro  
100 105 110

Val Leu Cys Gly Thr Ala Thr Gly Ser Leu Phe Ile Ala Lys Asp Asn  
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Gln Arg Gly Pro Gln Glu Ser Ser Phe Lys Asp Ala Lys His Pro Gln  
 130 135 140

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<210> 58  
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<400> 59

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24

&lt;210&gt; 60

&lt;211&gt; 62

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; PCR primer

&lt;400&gt; 60

cataatcaaa ctcaaagtca accatataag atctcctcct tacttcatga agaatcccct 60

cc

62

&lt;210&gt; 61

&lt;211&gt; 62

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; PRC primer

&lt;400&gt; 61

ggaggggatt cttcatgaag taaggaggag atcttatatg gttgactttg agtttgatta 60

tg

62

&lt;210&gt; 62

&lt;211&gt; 51

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; PCR primer

&lt;400&gt; 62

cgtgttactc attttgtctc ctggtcattt acttgaagtc tgctaagata c 51

&lt;210&gt; 63

&lt;211&gt; 51

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; PCR primer

&lt;400&gt; 63

gtatcttagc agacttcaag taaatgacga ggagacaaaa tgagtaacac g 51

&lt;210&gt; 64

&lt;211&gt; 60

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

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<212> DNA

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gactagatat ctcaggagta ctcattgggtg aa 32